SEQUENCE LISTING

<110> AMANO, Yuichiro SUGIYAMA, Yasuo NISHIDA, Mayumi TAKETOMI, Shigeh	nisa													
	Disease Model Animal Carrying Heterologous PPAR Alpha Gene Introduced Thereinto And Use Thereof													
<130> 2005-0041A/WMC/0	2005-0041A/wmc/00279													
<140> 10/521,174 <141> 2005-1-14														
<150> JP 2002-206162 <151> 2002-07-15														
<160> 9	9													
<170> PatentIn version	PatentIn version 3.1													
<210> 1 <211> 1404 <212> DNA <213> Homo sapiens	1404 DNA													
<220> <221> CDS <222> (1)(1404)														
<400> 1 atg gtg gac acg gaa ago Met Val Asp Thr Glu Ser 1 5	c cca ctc tgc ccc ctc tcc cca ctc gag gcc 48 Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala 10 15													
ggc gat cta gag agc ccg	g tta tct gaa gag ttc ctg caa gaa atg gga 96 b Leu Ser Glu Glu Phe Leu Gln Glu Met Gly 25 30													
aac atc caa gag att tcg	g caa tcc atc ggc gag gat agt tct gga agc 144 Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser 40 45													
ttt ggc ttt acg gaa tac	cag tat tta gga agc tgt cct ggc tca gat 192 Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp 55 60													
ggc tcg gtc atc acg gac Gly Ser Val Ile Thr Asp 65 70	acg ctt tca cca gct tcg agc ccc tcc tcg 240 Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser 75 80													
gtg act tat cct gtg gtc	ccc ggc agc gtg gac gag tct ccc agt gga 288 Pro Gly Ser Val Asp Glu Ser Pro Ser Gly 90 95													
gca ttg aac atc gaa tgt	aga atc tgc ggg gac aag gcc tca ggc tat 336 Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr 105 110													
cat tac gga gtc cac gcg	g tgt gaa ggc tgc aag ggc ttc ttt cgg cga 384 Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg 120 125													
acg att cga ctc aag ctg	gtg tat gac aag tgc gac cgc agc tgc aag 432 Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys 135 140													
atc cag aaa aag aac aga	aac aaa tgc cag tat tgt cga ttt cac aag 480 Asn Lys Cys Gln Tyr Cys Arg Phe His Lys													

tgc Cys	ctt Leu	tct Ser	gtc Val	ggg Gly 165	atg Met	tca Ser	cac His	aac Asn	gcg Ala 170	att Ile	cgt Arg	ttt Phe	gga Gly	cga Arg 175	atg Met	528
cca Pro	aga Arg	tct Ser	gag Glu 180	aaa Lys	gca Ala	aaa Lys	ctg Leu	aaa Lys 185	gca Ala	gaa Glu	att Ile	ctt Leu	acc Thr 190	tgt Cys	gaa Glu	576
cat His	gac Asp	ata Ile 195	gaa Glu	gat Asp	tct Ser	gaa Glu	act Thr 200	gca Ala	gat Asp	ctc Leu	aaa Lys	tct Ser 205	ctg Leu	gcc Ala	aag Lys	624
aga Arg	atc Ile 210	tac Tyr	gag Glu	gcc Ala	tac Tyr	ttg Leu 215	aag Lys	aac Asn	ttc Phe	aac Asn	atg Met 220	aac Asn	aag Lys	gtc Val	aaa Lys	672
gcc Ala 225	cgg Arg	gtc Val	atc Ile	ctc Leu	tca Ser 230	gga Gly	aag Lys	gcc Ala	agt Ser	aac Asn 235	aat Asn	cca Pro	cct Pro	ttt Phe	gtc Val 240	720
ata Ile	cat His	gat Asp	atg Met	gag Glu 245	aca Thr	ctg Leu	tgt Cys	atg Met	gct Ala 250	gag Glu	aag Lys	acg Thr	ctg Leu	gtg Val 255	gcc Ala	768
aag Lys	ctg Leu	gtg Val	gcc Ala 260	aat Asn	ggc Gly	atc Ile	cag Gln	aac Asn 265	aag Lys	gag Glu	gcg Ala	gag Glu	gtc Val 270	cgc	atc Ile	816
ttt Phe	cac His	tgc Cys 275	tgc Cys	cag Gln	tgc Cys	acg Thr	tca Ser 280	gtg Val	gag Glu	acc Thr	gtc Val	acg Thr 285	gag Glu	ctc Leu	acg Thr	864
gaa Glu	ttc Phe 290	gcc Ala	aag Lys	gcc Ala	atc Ile	cca Pro 295	ggc Gly	ttc Phe	gca Ala	aac Asn	ttg Leu 300	gac Asp	ctg Leu	aac Asn	gat Asp	912
caa Gln 305	gtg Val	aca Thr	ttg Leu	cta Leu	aaa Lys 310	tac Tyr	gga Gly	gtt Val	tat Tyr	gag Glu 315	gcc Ala	ata Ile	ttc Phe	gcc Ala	atg Met 320	960
ctg Leu	tct Ser	tct Ser	gtg Val	atg Met 325	aac Asn	aaa Lys	gac Asp	ggg Gly	atg Met 330	ctg Leu	gta Val	gcg Ala	tat Tyr	gga Gly 335	aat Asn	1008
ggg Gly	ttt Phe	ata Ile	act Thr 340	cgt Arg	gaa Glu	ttc Phe	cta Leu	aaa Lys 345	agc Ser	cta Leu	agg Arg	aaa Lys	ccg Pro 350	ttc Phe	tgt Cys	1056
gat Asp	atc Ile	atg Met 355	gaa Glu	ccc Pro	aag Lys	ttt Phe	gat Asp 360	ttt Phe	gcc Ala	atg Met	aag Lys	ttc Phe 365	aat Asn	gca Ala	ctg Leu	1104
gaa Glu	ctg Leu 370	gat Asp	gac Asp	agt Ser	gat Asp	atc Ile 375	tcc Ser	ctt Leu	ttt Phe	gtg Val	gct Ala 380	gct Ala	atc Ile	att Ile	tgc Cys	1152
tgt Cys 385	gga Gly	gat Asp	cgt Arg	cct Pro	ggc Gly 390	ctt Leu	Leu	Asn	Val	gga Gly 395	His	att Ile	gaa Glu	aaa Lys	atg Met 400	1200
cag Gln	gag Glu	ggt Gly	att Ile	gta Val 405	cat His	gtg Val	ctc Leu	aga Arg	ctc Leu 410	cac His	ctg Leu	cag Gln	agc Ser	aac Asn 415	cac His	1248
					ctc Leu											1296
			ctg		acg Thr			gcg					atc			1344
		gag			gct Ala		ctg					cag				1392
	gac Asp															1404

<210> 2 <211> 468 <212> PRT

<213> Homo sapiens

<400> Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala 10 Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser 35 40 45 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp 50 55 60 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser 65 70 75 80 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly 90 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr 105 His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg 115 120 125 Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys 135 Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys 145 150 155 160 15Ŏ Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met 165 170 175 Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu 180 185 190 His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys 200 205 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys 215 220 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val 235 230 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala 250 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile 265 270 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr 280 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp 295 300 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met 310 315 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn 325 330 335 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys 340 345 350 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu 360 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys 375 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met 385 390 395 400 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His 410 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp 425 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys 440 445 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr 450 455 Arg Asp Met Tyr

```
<210>
<211>
       20
<212>
       DNA
      Artificial Sequence
<213>
<220>
       Oligonucleotide designed to act as primer for amplifying human
<223>
       SAP promoter.
<400>
                                              20
actgagtaga agtagcagaa
<210>
       20
<211>
<212>
      DNA
      Artificial Sequence
<213>
<220>
<223>
       Oligonucleotide designed to act as primer for amplifying human
       SAP promoter.
<400>
cagcggcttg ttcatattcc
                                              20
<210>
       Ž9
<211>
<212>
      DNA
<213>
       Artificial Sequence
<220>
       Oligonucleotide designed to act as primer for amplifying rabbit
<223>
       beta-globin enhancer.
<400> 5
tcctaggtga gaacttcagg gtgagtttg
                                              29
<210>
       29
<211>
<212>
       DNA
<213> Artificial Sequence
<220>
<223>
       Oligonucleotide designed to act as primer for amplifying rabbit
       beta-globin enhancer.
                                              29
cggtaccttt gccaaaatga tgagacagc
<210>
       15
<211>
<212>
      Artificial Sequence
<213>
<220>
<223>
       Oligonucleotide designed to act as primer for amplifying human
       PPAR-alpha cDNA fragment.
<400>
                                              15
cgccagcacg gacga
<210>
      23
<211>
<212> DNA
<213> Artificial Sequence
```